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- (i) APPLICANT: Wackett, Lawrence P.
Sadowsky, Michael J.
de Souza, Mervyn L.
- (ii) TITLE OF INVENTION: An Isolated and Purified DNA Molecule
and Protein for the Degradation of Triazine Compounds
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
 - (B) STREET: P.O. Box 581415
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55458-1415
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mueting, Ann M.
 - (B) REGISTRATION NUMBER: 33,977
 - (C) REFERENCE/DOCKET NUMBER: 110.00230101
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-305-1217
 - (B) TELEFAX: 612-305-1228

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCGA GCATGGTGAC 60

CTTGACGCCG CTCTTTTCGT TCTCTTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT 120

GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT 180

TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA 240

AACGCTCAGC ATCCAGCACG GTACCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG 300

GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC 360

GGTGCCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCGGC AAGGTCGTGT TACCCGGTTT 420

CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG 480

TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCGA TGAGACCGGA 540

GGACGTAGCG GTGGCGGTGA GGTGTATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC 600

GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT 660

CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTTGATC GGATGGACGG 720

GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAAGTCG AACTGTGCTC 780

GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA 840

TGGCACGGCA GGAGGTCGTA TATCAGTTTG GCCCGCTCCT GCCACTACCA CGGCGGTGAC 900

AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT 960

TCACATGGCG GAGAGCGATC ATGATGAGCG GATTCATGGG ATGAGTCCCG CCGAGTACAT 1020

GGAGTGTTAC GGACTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG 1080

GAAGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA 1140

TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT 1200

GGGCATTGGA ACAGATAACG GGAATAGTAA TGA TCCGCA AACATGATCG GAGACATGAA 1260
 GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA 1320
 GATTCTTGAA ATGGCGACGA TCGATGGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG 1380
 TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG 1440
 ACTCTCACAT CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500
 TGTCTTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560
 ACGTGAGTTG GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC 1620
 GAACATGGTG GCTAACCCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680
 GCCGCCCCCTT GAGGAAATCG CTGCCATCTT GCGCGGCTC GGATTGGGGG GCGGACATGA 1740
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCATTCCG TCCTTCGCTC GTGTGGAATC 1800
 GTTGGTAGGT GAGGGTCGAC TCGGGCGCC AGCTTCCCGA AGAGGTGAAA GGCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5				10					15		
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20				25					30			
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
		35				40					45				
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
	50				55					60					
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
65				70				75					80		

Gly Arg Gln Phe Tyr Asp Trp Leu Phe Asn Val Val Tyr Pro Gly Gln
 85 90 95

Lys Ala Met Arg Pro Glu Asp Val Ala Val Ala Val Arg Leu Tyr Cys
 100 105 110

Ala Glu Ala Val Arg Ser Gly Ile Thr Thr Ile Asn Glu Asn Ala Asp
 115 120 125

Ser Ala Ile Tyr Pro Gly Asn Ile Glu Ala Ala Met Ala Val Tyr Gly
 130 135 140

Glu Val Gly Val Arg Val Val Tyr Ala Arg Met Phe Phe Asp Arg Met
 145 150 155 160

Asp Gly Arg Ile Gln Gly Tyr Val Asp Ala Leu Lys Ala Arg Ser Pro
 165 170 175

Gln Val Glu Leu Cys Ser Ile Met Glu Glu Thr Ala Val Ala Lys Asp
 180 185 190

Arg Ile Thr Ala Leu Ser Asp Gln Tyr His Gly Thr Ala Gly Gly Arg
 195 200 205

Ile Ser Val Trp Pro Ala Pro Ala Thr Thr Thr Ala Val Thr Val Glu
 210 215 220

Gly Met Arg Trp Ala Gln Ala Phe Ala Arg Asp Arg Ala Val Met Trp
 225 230 235 240

Thr Leu His Met Ala Glu Ser Asp His Asp Glu Arg Ile His Gly Met
 245 250 255

Ser Pro Ala Glu Tyr Met Glu Cys Tyr Gly Leu Leu Asp Glu Arg Leu
 260 265 270

Gln Val Ala His Cys Val Tyr Phe Asp Arg Lys Asp Val Arg Leu Leu
 275 280 285

His Arg His Asn Val Lys Val Ala Ser Gln Val Val Ser Asn Ala Tyr
 290 295 300

Leu Gly Ser Gly Val Ala Pro Val Pro Glu Met Val Glu Arg Gly Met
 305 310 315 320

Ala Val Gly Ile Gly Thr Asp Asn Gly Asn Ser Asn Asp Ser Ala Asn
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Met Ile Gly Asp Met Lys Phe Met Ala His Ile His Arg Ala Val His
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Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr
 355 360 365
 Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile
 370 375 380
 Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Leu
 385 390 395 400
 Arg Arg Leu Ser His His Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr
 405 410 415
 Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met Glu
 420 425 430
 Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu
 435 440 445
 Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met
 450 455 460
 Val Ala Asn Pro Ala Trp Arg Ser Leu
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